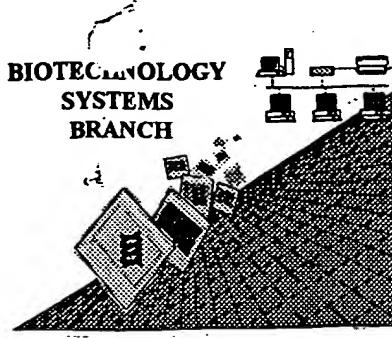


## RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/914,220

Source: Put/s9

Date Processed by STIC: 9/14/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:  
<http://www.uspto.gov/web/offices/pac/checker>

PCT09

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/914,220

DATE: 09/14/2001  
TIME: 10:39:35

Input Set : A:\Debelseq.txt  
Output Set: N:\CRF3\09142001\I914220.raw

Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: Schulz Dr., Burkhard  
5 <120> TITLE OF INVENTION: DNA sequence of a protein that is similar to FKBP  
7 <130> FILE REFERENCE: SCU-001 PCT  
9 <140> CURRENT APPLICATION NUMBER: US/09/914,220  
10 <141> CURRENT FILING DATE: 2001-08-22  
12 <150> PRIOR APPLICATION NUMBER: DE 199 07 598.0  
13 <151> PRIOR FILING DATE: 1999-02-22  
15 <160> NUMBER OF SEQ ID NOS: 8  
17 <170> SOFTWARE: PatentIn Ver. 2.1

## ERRORED SEQUENCES

309 <210> SEQ ID NO: 7  
310 <211> LENGTH: 776  
311 <212> TYPE: DNA  
312 <213> ORGANISM: Zea mays  
314 <400> SEQUENCE: 7  
315 tttttttttt tttttccccc tagcaacagt attattacta gcataatcta aatatgaaag 60  
316 ctgcaataata caatggcata aaaggccott tgagctccag ttgaaagact gtatgaaact 120  
317 atggcataata agtgaacaac atcgatataga gttcataaca actaatttgat ccggaccggc 180  
318 cgacagttct acagaaaatt caacactct tataatacaa ggttggtcaa ttaggccacc 240  
319 agttctacac aattttctgg taaattatcc tactcggtct tccgtttgaa catcccagcc 300  
320 agataaaagga taaatgacac cagccactgc cagaacacaa cgaggtactt tgcccttctc 360  
321 gtttgcgtt caggacttgg cccaaagaga cctttaga gtccttctq ctttggat 420  
E--> 322 agggccttgn cttgtccgc gagcaaacgg agctccgaa tgatctcctt gncttctgg 480  
323 gagtacttct tcgetttgag gaaatcttcc ctcgctgatt ctgtctggcc aagttcagat 540  
324 ttagctttc ctcgcctgaa cagcgcttgc acattactt catcttctgt caaaacaatg 600  
325 ctacactgcg caatagcttc atcgaatctc tttagttga tcaggcatgc ggcattattg 660  
326 agatggcatg gattttcac agccaaggcc atgtctctgt actttccaaa taattgaaac 720  
327 atgaaatcat ctcccatgtt tgcaatcgcc atttcattt gctgcattggc ctcctc 776  
330 <210> SEQ ID NO: 8  
331 <211> LENGTH: 168  
332 <212> TYPE: PRT  
333 <213> ORGANISM: Zea mays  
335 <400> SEQUENCE: 8  
336 Glu Glu Ala Met Gln Gln Tyr Glu Met Ala Ile Ala Tyr Met Gly Asp  
337 1 5 10 15  
339 Asp Phe Met Phe Gln Leu Phe Gly Lys Tyr Arg Asp Met Ala Leu Ala  
340 20 25 30  
342 Val Lys Asn Pro Cys His Leu Asn Met Ala Ala Cys Leu Ile Lys Leu  
343 35 40 45  
345 Lys Arg Phe Asp Glu Ala Ile Ala Gln Cys Ser Ile Val Leu Thr Glu  
346 50 55 60  
348 Asp Glu Ser Asn Val Lys Ala Leu Phe Arg Arg Gly Lys Ala Lys Ser  
349 65 70 75 80  
351 Glu Leu Gly Gln Thr Glu Ser Ala Arg Glu Asp Phe Leu Lys Ala Lys

P.2

> see  
item 9  
in Error  
summary  
sheet

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/914,220

DATE: 09/14/2001  
TIME: 10:39:35

Input Set : A:\Debelseq.txt  
Output Set: N:\CRF3\09142001\I914220.raw

352                    85                    90                    95  
E--> 354 Lys Tyr Ser Pro Glu Xaa Lys Glu Ile Ile Arg Glu Leu Arg Leu Leu  
355                    100                    105                    110  
E--> 357 Ala Glu Gln Xaa Lys Ala Leu Tyr Gln Lys Gln Lys Glu Leu Tyr Lys  
358                    115                    120                    125                    Item 9  
360 Gly Leu Phe Gly Pro Ser Pro Glu Ala Lys Pro Lys Lys Ala Lys Tyr  
361                    130                    135                    140  
363 Leu Val Val Phe Trp Gln Trp Leu Val Ser Phe Ile Leu Tyr Leu Ala  
364 145                    150                    155                    160  
366 Gly Met Phe Lys Arg Lys Asn Glu  
367                    165

**Raw Sequence Listing Error Summary**

<b>ERROR DETECTED</b>	<b>SUGGESTED CORRECTION</b>	<b>SERIAL NUMBER: 09/914,220</b>
<b>ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE</b>		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	